REPORTER'S RECORD

VOLUME 2 OF 3

TRIAL COURT CASE NO. 5216

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| STATE OF TEXAS | ) | IN THE DISTRICT COURT |
| | ) | |
| VS. | ) | GRAY COUNTY, TEXAS |
| | ) | |
| HENRY WATKINS SKINNER | ) | 31ST JUDICIAL DISTRICT |

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EVIDENTIARY HEARING

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On the 9th day of January, 2018, the following proceedings came on to be heard in the above-entitled and numbered cause before the Honorable Steven Emmert, Judge Presiding, in the District Court, Gray County, Pampa, Texas:

Proceedings reported by machine shorthand.

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A. Well, if you are looking at a two-person mixture, that has 0.125 nanograms of DNA amplified. And if you're looking at that in a 20 to 1 mixture ratio, you would expect, you sum those together, those numbers together so that would be 1 over 21 and then multiply that by 0.125 or we could defer it to picograms and just call it 125 picograms. So there would be approximately 6 picograms from a minor contributor evaluated under a 20 to 1 mixture ratio at 125.

Q. And how does that compare to the other numbers that you observed or calculated in the items of interest with respect to the amount of template DNA that was present for those items?

A. Those line up with -- with some of the inferences we've made from STRmix's output.

Q. I'm sorry. I don't understand your answer. Could you -- could you tell me in what way they line up? What do you mean by that?

A. Oh, there's a range of values that based on the calculations I did on that worksheet, that assuming there is a minor contributor in that mixture, there's a variation in the amounts of -- they change by a bit. They go down as low -- they go down to about a picogram on that worksheet and up to several dozen picograms, I believe. And that is represented by some of the mixtures that DPS evaluated in the two-person STRmix validation, internal validation.

Q. Is it represented by all of the mixtures that DPS or even the majority of the mixtures that DPS used in their validation studies?

A. Those extreme mixtures that -- that we've been looking at in this case are on the small end of what DPS considered in their validation studies.

Q. Does it matter that DPS conducted it's internal validation studies with STRmix using different template amounts than the ones that are estimated for our items of interest?

A. We're -- it's more informative as to the expectations of how STRmix would perform if we're comparing casework samples the more closely they resemble the evaluations performed during the validation studies, the more confident we can feel in those conclusions.

Q. According to the research and the scientific literature that you are familiar with, how does STRmix behave when it's evaluating DNA samples where the template amounts are very small? Is there any observed effect on the operation of STRmix from it's evaluation of really really small amounts of DNA?

A. Well, our expectation with small amounts of DNA is that any signal produced by that contribution is going to be very small, which is associated with greater uncertainty about the origin of that DNA in terms of

genotype, in terms of contributor quantity. There's a lot of complications going into such an interpretation. So we would expect conclusions -- statistical conclusions about those various explanations to be more diffuse, to be less certain about particular explanations. And that means the likelihood ratios tend to trend towards 1 the smaller amount of DNA that goes into a mixture evaluated by STRmix.

Q. And this may be a different way of captioning what you just said. But let me ask if this is a correct understanding that one of the ways in which one might observe this behavior of STRmix is greater variability in the likelihood ratios that it outputs if it is examining smaller amounts of DNA material?

A. To look at that, we could run STRmix repeatedly variations across repeat runs of STRmix. But within one run we would generally expect the probabilities to be more spread out amongst more possible genotypes.

Q. I'm going to talk about another factor that might be in play with respect to the samples of interest in this case. What does it mean to say that a DNA sample has undergone degradation?

A. Degradation is going to be the breaking of the DNA molecules such that they can't be reliably genotyped and that is typically associated with a greater loss of larger DNA molecules. So if we're looking at an electropherogram we

would experience less loss from degradation on the shorter molecules to the left side of the electropherogram and more loss of those peaks to the right side of the electropherogram.

Q. What types of factors could contribute to degradation?

A. Environmental factors?

Q. Yeah.

A. So increased moisture and UV light. DNA will degrade over time, but it is accelerated by the environmental factors; heat and moisture, light.

Q. Were you aware of any laboratories which when conducting internal validation studies for probabilistic genotyping software have intentionally degraded samples in order to see how the software reacts when it's working with degraded samples?

A. The New York OCME intentionally degraded some of their samples.

Q. Are you aware of what -- what their observations were about how STRmix behaved in processing those kinds of samples?

A. Sorry that was for their forensic statistical tool validation that -- that I read that. They ultimately removed the degradation selector, there is no longer the option. After conducting that study, they didn't include

Mr. Ottoway calls it, is irrelevant to whether you can read this output or not. And Mr. Adams also said that his daily job tasks include reading electropherograms and studying electropherograms and comparing them to other electropherograms. And I think if the Court wants to weigh how much weight to give his testimony on this point after he's been cross examined, certainly you can do that. But I don't think that the State has established he shouldn't be allowed to testify.

THE COURT: Okay. You may proceed. Go ahead.

DIRECT EXAMINATION (CONT)

BY MR. OWEN:

Q. Mr. Adams, I was asking you to take a look at this electropherogram we were just referring to D47 -- DX 47 at page 8. And tell us what you see there, if anything, that might show reason to question the explanation we just read for calling this sample a mixture of two persons?

A. Well, it -- excuse me. At D8 we see two tall peaks that labels with 10 and 14.

Q. Mr. Adams, I'm going to stop you for just a second to make sure that the Court and the State are on the same page where we are. But we're at the top of these three boxes on page 8; is that correct?

A. Yes.

Q. And when you say we're at D8, looking at D8,

where is that?

A. That's the -- the first locus. That's the area covered by the first green bar on the top row.

Q. And does it say D8 on there for reference purposes?

A. It does on the green bar. This reproduction also has D8 typed below the labels that I was just referencing.

Q. Okay. I'm sorry to interrupt you. If you can continue. I appreciate it.

A. So the -- the labels associated with 10 and 14, these two peaks at 10 and 14 have RFU values of over 1000 and there are two peaks to the left of each of those two tall peaks, exactly one repeat shorter, so 9 has a peak height of 123 compared to that 10's peak height of 1,927. So the 9 is in position to be considered minus stutter. And that 13 with a height of 91 is in a similar position to the 14 and considered minus stutter off of that 14 peak.

Q. Could you explain to the Court what minus stutter is. What is stutter in that electropherogram?

A. Stutter is a product of the amplification process where there is a contribution of actual allelic material associated with, in this case it would be associated with the 10 and the 14 peaks. During the amplification process, there can be an artifact produced where a shorter

peak or a taller peak -- a taller -- it's really a longer or a shorter amplified sequence of DNA is recorded. So this peak that's in the 9 position could be a product of that -- that artifact of the amplification process as opposed to being a 9 from an actual human being an actual contributor to a sample. So this is one of the considerations, that STRmix does the evaluation of the -- the minus stutter peaks. However, the -- so the 9 and the 13 they might be explained by this -- this minus stutter explanation. But that 11 is not in a minus stutter position to any tall peak. So it could be from a real contributor. It is, however, in the plus stutter position to this 10 peak. And it's small size relative small height, relative to that 10 peak is -- is somewhere in the area that we would expect plus stutter to be approximately.

Q. What's that -- what's that range for a plus stutter?

A. It's generally around 1 to 3 percent. Minus stutter is typically associated with taller peaks. So those might be in the 10 or 15 percent range up to that height. Another explanation for that 11 peak, I suppose, could drop in -- drop-in peaks.

Q. Would you tell us what drop-in is please?

A. It is -- it's technically contamination, but it is generally considered to be contamination that's only

occurring at a single locus. That it is not associated with a contamination of an entire profile. It's a straight piece of genetic material that somehow got into the sample that's not associated with a full contributor to the sample. And since it is a straight piece of genetic material it is typically not associated with very tall peak heights. So there's a variety of explanations that could be given for that 11, one of which requires it to be a two-person mixture, but the other two do not necessarily.

Q. Was the version of STRmix that was used in this case version 2.3.07, was it capable of contributing any of this observed data to a plus or forward stutter?

A. Not this version of STRmix.

Q. And -- and that's because it just didn't have it as part of its program? It wasn't programmed to do that?

A. It was added in a later version of STRmix.

Q. Okay. Has Texas DPS Lab set any parameter for STRmix that affected the ability of the program to attribute any of the observed data to drop-in which you mentioned earlier?

A. Yeah, this -- this version of STRmix used in this case was capable of evaluating drop-in, but DPS set their drop-in parameters to zero. It -- it didn't allow an attribution of observed DNA to the --

Q. Possibility of a drop-in?

A. -- the explanation of drop-in, yes, sir.

Q. Did those two considerations, the absence of the ability of the program to take account of positive stutter as a possible explanation and the setting of the drop-in cap at zero, did those things constrain the analysis that STRmix was able to perform?

A. Yes.

Q. In what way?

A. It required an attribution of that 11 to a second contributor.

Q. So STRmix in that sense had no other option to then to call it a mixture or to attempt to explain the data for -- as a -- as a mixture, is that right?

A. None that I can think of and none that was reported.

Q. By the way, what does it mean to attribute the purported extra allele at D8 to a lower threshold? That phrase "lower threshold" was in the notes that I -- that I mentioned that we saw in Mr. Hester's worksheet. What did -- what threshold are we talking about and how did it get lower?

A. It -- it seems to be talking about the analytical threshold. There were earlier printouts of this electropherogram that didn't have this 11 peak present. And it's my understanding that this is the lowering of the analytical threshold, that's the noise threshold for